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=> d his

     (FILE 'AGRICOLA, CAPLUS, BIOSIS' ENTERED AT 18:29:50 ON 07 DEC 2004)
               DEL HIS

     FILE 'CAPLUS' ENTERED AT 18:32:31 ON 07 DEC 2004
L1           368 S SEED (4A) SPECIFIC (5A) PROMOTER
L2           263 S L1 AND (NUCLEOTIDE SEQUENCE OR DNA)
L3           181 S L2 AND PLANT(4A)(TRANSFORM? OR TRANSGEN?)
L4             6 S L3(5A)(ARABIOPSIS THALIANA OR A. THALIANA)
L5             6 S L3 AND (ARABIOPSIS THALIANA OR A. THALIANA)
L6             6 S L4 OR L5
               SAV OHLR059/A L6

     FILE 'BIOSIS' ENTERED AT 19:33:13 ON 07 DEC 2004

     FILE 'AGRICOLA' ENTERED AT 19:33:25 ON 07 DEC 2004

     FILE 'BIOSIS, AGRICOLA' ENTERED AT 19:33:48 ON 07 DEC 2004
L7             0 FILE BIOSIS
L8             0 FILE AGRICOLA
     TOTAL FOR ALL FILES
L9             0 S SEED(4A)PROMOTER(5A)(DNA OR NUCLEOTIDE SEQUENCE) AND PLANT(4A
L10            8 FILE BIOSIS
L11           13 FILE AGRICOLA
     TOTAL FOR ALL FILES
L12           21 S SEED(4A)PROMOTER AND (DNA OR NUCLEOTIDE SEQUENCE) AND PLANT(4

     FILE 'CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 19:37:30 ON 07 DEC 2004
L13           24 DUP REM L6 L12 (3 DUPLICATES REMOVED)

=> d ibib abs total

L13  ANSWER 1 OF 24  BIOSIS  COPYRIGHT (c) 2004 The Thomson Corporation.  on
     STN
ACCESSION NUMBER:    2004:47478  BIOSIS
DOCUMENT NUMBER:     PREV200400040141
TITLE:               Synthesis of ketocarotenoids in the seed of
                     Arabidopsis thaliana.
AUTHOR(S):           Stalberg, Kjell [Reprint Author]; Lindgren, Ove; Ek, Bo;
                     Hoglund, Anna-Stina
CORPORATE SOURCE:    Department of Plant Biology and Forest Genetics, Swedish
                     University of Agricultural Science, 750 07, Box 7080,
                     Uppsala, Sweden
                     kjells@mail1.slu.se
SOURCE:              Plant Journal, (December 2003) Vol. 36, No. 6, pp. 771-779.
                     print.
                     ISSN: 0960-7412 (ISSN print).
DOCUMENT TYPE:       Article
LANGUAGE:            English
ENTRY DATE:          Entered STN: 14 Jan 2004
                     Last Updated on STN: 14 Jan 2004
AB   A cDNA coding for a gene necessary for synthesis of ketocarotenoids was
     cloned from the alga Haematococcus pluvialis and expressed in the seed of
     Arabidopsis thaliana.  The expression of the algal
     beta-carotene-oxygenase gene was directed to the seed by use of the 2S,
     seed storage protein promoter napA.  Extracts from seeds
     of the transgenic plants were clearly red because of
     accumulation of ketocarotenoids, and free and esterified forms of
     ketocarotenoids were found in addition to the normal carotenoid
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composition in the seed. The major ketocarotenoids in the **transgenic plants** were: 4-keto-lutein (3,3'-dihydroxy-beta-,epsilon-carotene-4-one), adonirubin (3-hydroxy-beta-,beta'-carotene-4,4'-dione) and canthaxanthin (beta-,beta'-carotene-4,4'-dione). 4-Keto-lutein differs from the more common adonixanthin only in the position of one double bond. To increase the substrate availability for the beta-carotene-oxygenase, these **transformants** were crossed with **transgenic plants** overexpressing a construct of an endogenous phytoene synthase gene, also under the control of the napA promoter. The resulting crossings gave rise to seeds with a 4.6-fold relative increase of the total pigment, and the three major ketocarotenoids were increased 13-fold compared to seeds of **transgenic plants** carrying only the beta-carotene-oxygenase construct.

L13 ANSWER 2 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:137189 CAPLUS
DOCUMENT NUMBER: 138:334400
TITLE: Biochemical and physiological studies of Arabidopsis thaliana transgenic lines with repressed expression of the mitochondrial pyruvate dehydrogenase kinase
AUTHOR(S): Marillia, Elizabeth-France; Micallef, Barry J.; Micallef, Malgre; Weninger, Alan; Pedersen, Kalie K.; Zou, Jitao; Taylor, David C.
CORPORATE SOURCE: Plant Biotechnology Institute, National Research Council of Canada, Saskatoon, SK, S7N 0W9, Can.
SOURCE: Journal of Experimental Botany (2003), 54(381), 259-270
CODEN: JEBOA6; ISSN: 0022-0957
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Pyruvate dehydrogenase kinase (PDHK), a neg. regulator of the mitochondrial pyruvate dehydrogenase complex (mtPDC), plays a pivotal role in controlling mtPDC activity, and hence, the TCA cycle and cell respiration. Previously, the cloning of a PDHK cDNA from Arabidopsis thaliana and the effects of constitutively down-regulating its expression on plant growth and development has been reported. The first detailed analyses of the biochem. and physiol. effects of partial silencing of the mtPDHK in **A. thaliana** using antisense constructs driven by both constitutive and **seed-specific promoters** are reported here. The studies revealed an increased level of respiration in leaves of the constitutive antisense PDHK transgenics; an increase in respiration was also found in developing seeds of the seed-specific antisense transgenics. Both constitutive and seed-specific partial silencing of the mtPDHK resulted in increased seed oil content and seed weight at maturity. Feeding 3-14C pyruvate to bolted stems containing siliques (constitutive transgenics), or to isolated siliques or immature seeds (seed-specific transgenics) confirmed a higher rate of incorporation of radiolabel into all seed lipid species, particularly triacylglycerols. Neither constitutive nor seed-specific partial silencing of PDHK neg. affected overall silique and seed development. Instead, oil and seed yield, and overall plant productivity were improved. These findings suggest that a partial reduction of the repression of the mtPDC by antisense PDHK expression can alter carbon flux and, in particular, the contribution of carbon moieties from pyruvate to fatty acid biosynthesis and storage lipid accumulation in developing seeds, implicating a role for mtPDC in fatty acid biosynthesis in seeds.
REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 3 OF 24 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
ACCESSION NUMBER: 2003:239758 BIOSIS
DOCUMENT NUMBER: PREV200300239758
TITLE: Repression of gene expression by **Arabidopsis** HD2 histone deacetylases.
AUTHOR(S): Wu, Keqiang [Reprint Author]; Tian, Lining; Zhou, Changhe; Brown, Daniel; Miki, Brian
CORPORATE SOURCE: Department of Biology, West Virginia University, Morgantown, WV, 26506, USA
kewu@mail.wvu.edu
SOURCE: Plant Journal, (April 2003) Vol. 34, No. 2, pp. 241-247. print.
ISSN: 0960-7412 (ISSN print).
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 21 May 2003
Last Updated on STN: 21 May 2003

AB The four HD2 proteins of **Arabidopsis** thaliana (AtHD2A-D) belong to a unique class of histone deacetylases that is plant specific. Previously, we have demonstrated that one of the members, AtHD2A, can mediate transcriptional repression when targeted to the promoter of a reporter gene. Here, we report that AtHD2B and AtHD2C can also repress gene expression. AtHD2A and AtHD2C differ from AtHD2B and AtHD2D in the composition of their structural domains. Our data show that both structural types play a role in the repression of gene transcription. We demonstrate that AtHD2A can mediate gene repression through interactions with transcription factors in plants. By fusing AtHD2A with the **DNA**-binding domain of the plant transcriptional factor Pti4, the expression of a GCC box containing reporter gene was repressed. We also demonstrated repression of a GUS gene with GAL4 enhancers using **transgenic plants** that expressed a GAL4/AtHD2A fusion gene. Furthermore, the expression of the GAL4/AtHD2A protein using the **seed**-specific napin **promoter** (NAP2) and the constitutive tCUP promoter demonstrated that repression of transgenes could be achieved in a tissue-specific or unrestricted manner. Targeting of HD2 proteins to specific promoters using transcription factor **DNA**-binding domains may therefore provide a new technology for silencing target genes and pathways in plants as well as for assessing the function of unknown transcription factors.

L13 ANSWER 4 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
ACCESSION NUMBER: 2003:34615 AGRICOLA
DOCUMENT NUMBER: IND23324092
TITLE: Regulation and role of the **Arabidopsis** abscisic acid-insensitive 5 gene in abscisic acid, sugar, and stress response.
AUTHOR(S): Brocard, I.M.; Lynch, T.J.; Finkelstein, R.R.
AVAILABILITY: DNAL (450 P692)
SOURCE: Plant physiology, Aug 2002. Vol. 129, No. 4. p. 1533-1543
Publisher: Rockville, MD : American Society of Plant Physiologists, 1926-
CODEN: PLPHAY; ISSN: 0032-0889
NOTE: Includes references
PUB. COUNTRY: Maryland; United States

DOCUMENT TYPE: Article; Conference
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English
AB Abscisic acid (ABA) and stress response from late embryonic growth through early seedling development is regulated by a signaling network that includes the **Arabidopsis** ABA-insensitive (ABI)5 gene, which encodes a basic leucine zipper transcription factor. We have characterized genetic, developmental, and environmental regulation of ABI5 expression. Although expressed most strongly in **seeds**, the ABI5 **promoter** is also active in vegetative and floral tissue. Vegetative expression is strongly induced by ABA, and weakly by stress treatments during a limited developmental window up to approximately 2 d post-stratification, but ABA and some stresses can induce expression in specific tissues at later stages. ABI5 expression is autoregulated in **transgenic plants** and yeast (Saccharomyces cerevisiae), and stress response appears to involve ABI5-dependent and -independent mechanisms. To determine whether ABI5 is necessary and/or sufficient for ABA or stress response, we assayed the effects of increased ABI5 expression on growth and gene expression. Although overexpression of ABI5 confers hypersensitivity to ABA and sugar, as previously described for ABI4 and ABI3 overexpression lines, it has relatively limited effects on enhancing ABA-responsive gene expression. Comparison of expression of eight ABI5-homologous genes shows overlapping regulation by ABI3, ABI4, and ABI5, suggestive of a combinatorial network involving positive and negative regulatory interactions.

L13 ANSWER 5 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
ACCESSION NUMBER: 2003:23356 AGRICOLA
DOCUMENT NUMBER: IND23315200
TITLE: Guard cell- and phloem idioblast-specific expression of thioglucoside glucohydrolase 1 (Myrosinase) in **Arabidopsis.**
AUTHOR(S): Husebye, H.; Chadchawan, S.; Winge, P.; Thangstad, O.P.; Bones, A.M.
AVAILABILITY: DNAL (450 P692)
SOURCE: Plant physiology, Apr 2002. Vol. 128, No. 4. p. 1180-1188
Publisher: Rockville, MD : American Society of Plant Physiologists, 1926-
CODEN: PLPHAY; ISSN: 0032-0889
NOTE: Includes references
PUB. COUNTRY: Maryland; United States
DOCUMENT TYPE: Article; Conference
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English
AB Thioglucoside glucohydrolase 1 (TGG1) is one of two known functional myrosinase enzymes in **Arabidopsis.** The enzyme catalyzes the hydrolysis of glucosinolates into compounds that are toxic to various microbes and herbivores. **Transgenic Arabidopsis plants** carrying beta-glucuronidase and green fluorescent protein reporter genes fused to 0.5 or 2.5 kb of the TGG1 promoter region were used to study spatial promoter activity. Promoter activity was found to be highly specific and restricted to guard cells and distinct cells of the phloem. No promoter activity was detected in the root or **seed.** All guard cells show **promoter** activity. Positive phloem cells are distributed in a discontinuous pattern and occur more frequent in young tissues. Immunocytochemical localization of myrosinase in transverse

and longitudinal sections of embedded material show that the TGG1 promoter activity reflects the position of the myrosinase enzyme. In the flower stalk, the myrosinase-containing phloem cells are located between phloem sieve elements and glucosinolate-rich S cells. Our results suggest a cellular separation of myrosinase enzyme and glucosinolate substrate, and that myrosinase is contained in distinct cells. We discuss the potential advantages of locating defense and communication systems to only a few specific cell types.

L13 ANSWER 6 OF 24 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 1

ACCESSION NUMBER: 2002:384555 BIOSIS
DOCUMENT NUMBER: PREV200200384555
TITLE: A soybean lectin-GFP fusion labels the vacuoles in developing **Arabidopsis** thaliana embryos.
AUTHOR(S): Darnowski, D. W.; Vodkin, L. O. [Reprint author]
CORPORATE SOURCE: Department of Crop Sciences, University of Illinois at Urbana-Champaign, Urbana, IL, 61801, USA
l-vodkin@uiuc.edu
SOURCE: Plant Cell Reports, (May, 2002) Vol. 20, No. 11, pp. 1033-1038. print.
CODEN: PCRPD8. ISSN: 0721-7714.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 10 Jul 2002
Last Updated on STN: 10 Jul 2002

AB We report the use of a derivative of the green fluorescent protein (GFP) to directly label the plant vacuole in live, unfixed tissues of stably **transformed transgenic plants.** We used the developmentally regulated soybean **seed** lectin **promoter** and the 32 amino acids of the soybean lectin amino terminal signal sequence to create an in-frame fusion polypeptide with GFP (pLGFP5). This construct was transferred into **Arabidopsis** thaliana by vacuum infiltration, and the transformed lines were characterized by **DNA** blotting and immunoblotting to detect the presence and expression of the GFP gene. GFP fluorescence was detected in the protein storage vacuoles of developing **Arabidopsis** embryos as imaged by fluorescence microscopy. Very little signal was detected in any other compartments including the cell wall. Thus, despite the absence of vacuolar sorting signals in GFP and other foreign proteins fused to the lectin sequence, the 32-amino-acid lectin signal sequence has general utility to direct foreign proteins to the protein storage vacuoles in seeds.

L13 ANSWER 7 OF 24 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN

ACCESSION NUMBER: 2002:545158 BIOSIS
DOCUMENT NUMBER: PREV200200545158
TITLE: Cotton alpha-globulin promoter: Isolation and functional characterization in transgenic cotton, **Arabidopsis** , and tobacco.
AUTHOR(S): Sunilkumar, Ganesan; Connell, James P.; Smith, C. W.; Reddy, Avutu S.; Rathore, Keerti S. [Reprint author]
CORPORATE SOURCE: Institute for Plant Genomics and Biotechnology, Texas A and M University, College Station, TX, 77843-2123, USA
rathore@tamu.edu
SOURCE: Transgenic Research, (August, 2002) Vol. 11, No. 4, pp. 347-359. print.
ISSN: 0962-8819.
DOCUMENT TYPE: Article
LANGUAGE: English

ENTRY DATE: Entered STN: 23 Oct 2002
Last Updated on STN: 23 Oct 2002

AB Globulins are the most abundant seed storage proteins in cotton and, therefore, their regulatory sequences could potentially provide a good source of **seed**-specific **promoters.** We isolated the putative promoter region of cotton alpha-globulin B gene by gene walking using the primers designed from a cotton staged embryo cDNA clone. PCR amplified fragment of 1108 bp upstream sequences was fused to gusA gene in the binary vector pBI101.3 to create the test construct. This was used to study the expression pattern of the putative promoter region in transgenic cotton, **Arabidopsis**, and tobacco. Histochemical GUS analysis revealed that the promoter began to express during the torpedo stage of seed development in tobacco and **Arabidopsis**, and during cotyledon expansion stage in cotton. The activity quickly increased until embryo maturation in all three species. Fluorometric GUS analysis showed that the promoter expression started at 12 and 15 dpa in tobacco and cotton, respectively, and increased through seed maturation. The strength of the promoter expression, as reflected by average GUS activity in the seeds from primary **transgenic plants**, was vastly different amongst the three species tested. In **Arabidopsis**, the activity was 16.7% and in tobacco it was less than 1% of the levels detected in cotton seeds. In germinating seedlings of tobacco and **Arabidopsis**, GUS activity diminished until it was completely absent 10 days post imbibition. In addition, absence of detectable level of GUS expression in stem, leaf, root, pollen, and floral bud of transgenic cotton confirmed that the **promoter** is highly **seed**-specific. Analysis of GUS activity at individual seed level in cotton showed a gene dose effect reflecting their homozygous or hemizygous status. Our results show that this promoter is highly tissue-specific and it can be used to control transgene expression in dicot seeds.

L13 ANSWER 8 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:168132 CAPLUS
DOCUMENT NUMBER: 134:218021
TITLE: Nucleic acids encoding plant sterol acyltransferases and their use to modify sterol composition
INVENTOR(S): Lassner, Michael; Van Eenennaam, Alison
PATENT ASSIGNEE(S): Monsanto Company, USA
SOURCE: PCT Int. Appl., 127 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001016308	A2	20010308	WO 2000-US23863	20000830
WO 2001016308	A3	20020117		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2381901	AA	20010308	CA 2000-2381901	20000830

BR 2000014154	A	20020507	BR 2000-14154		20000830
EP 1210417	A2	20020605	EP 2000-959644		20000830
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL					
JP 2003508052	T2	20030304	JP 2001-520855		20000830
ZA 2002001410	A	20030606	ZA 2002-1410		20020219
PRIORITY APPLN. INFO.:			US 1999-152493P	P	19990830
			WO 2000-US23863	W	20000830

AB The present invention is directed to lecithin:cholesterol acyltransferase-like polypeptides (LCAT) and acyl CoA:cholesterol acyltransferases-like polypeptides (ACAT). The invention provides polynucleotides encoding such cholesterol:acyltransferase-like polypeptides, polypeptides encoded by such polynucleotides, and the use of such polynucleotides to alter sterol composition and oil production in plants and host cells. Four LCAT cDNAs are provided from Arabidopsis thaliana, as well as 2 genomic **DNAs** encoding LCAT from **A. thaliana**, 7 ESTs from soybean and 11 ESTs from corn. ACAT-encoding ESTs are also identified from **A. thaliana**, soybean, maize, and Mortierella alpina. Also provided are oils produced by the plants and host cells containing the polynucleotides and food products, nutritional supplements, and pharmaceutical composition containing plants or oils of the present invention.

L13 ANSWER 9 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN

ACCESSION NUMBER:	2001:57453 AGRICOLA
DOCUMENT NUMBER:	IND23216261
TITLE:	Transgenic expression of a delta12-epoxygenase gene in **Arabidopsis** seeds inhibits accumulation of linoleic acid.
AUTHOR(S):	Singh, S.; Thomaeus, S.; Lee, M.; Stymne, S.; Green, A.
AVAILABILITY:	DNAL (450 P693)
SOURCE:	Planta, Apr 2001. Vol. 212, No. 5/6. p. 872-879 Publisher: Berlin ; New York : Springer-Verlag, 1925- CODEN: PLANAB; ISSN: 0032-0935
NOTE:	Includes references
PUB. COUNTRY:	Germany
DOCUMENT TYPE:	Article
FILE SEGMENT:	Non-U.S. Imprint other than FAO
LANGUAGE:	English

AB The Crepis palaestina cDNA Cpal2 encodes a delta12-epoxygenase that can catalyse the synthesis of 12,13-epoxy-cis-9-octadecenoic acid (18:1E) from linoleic acid (18:2). When the Cpal2 gene was expressed under the control of the napin **seed**-specific **promoter** in **Arabidopsis** thaliana (L.) Heynh., the seed lipids accumulated only low levels of 18:1E and also 12,13-epoxy-cis-9,15-octadec-2-enoic acid (18:2E). Despite the fact that the levels of these epoxy fatty acids comprised only up to 6.2% of the total fatty acids, there was a very marked increase in oleic acid (18:1) and decrease in linoleic (18:2) and alpha-linolenic (18:3) acids in these plants, indicating that endogenous delta12-desaturation was greatly reduced in these plants. Significant between-line differences in the levels of Cpal2 mRNA were observed during seed development, but were not associated with any major variation in mRNA levels for the endogenous **Arabidopsis** delta12-desaturase (Fad2). This suggests that if an unfavourable interaction occurs between the

transgenic delta12-epoxygenase and the endogenous delta12-desaturase, which decreases the level of desaturation, it occurs at either the translational or post-translational level. We further show that the co-expression of a delta12-desaturase gene from C. palaestina in Cpal2 transgenic **Arabidopsis** returns the relative proportions of the C18 seed fatty acids to normal levels and results in an almost twofold increase in total epoxy fatty acids.

L13 ANSWER 10 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN

ACCESSION NUMBER: 2002:26210 AGRICOLA
DOCUMENT NUMBER: IND23261242
TITLE: Expression of the FAE1 gene and FAE1 **promoter** activity in developing **seeds** of **Arabidopsis** thaliana.
AUTHOR(S): Rossak, M.; Smith, M.; Kunst, L.
AVAILABILITY: DNAL (QK710.P62)
SOURCE: Plant molecular biology, Aug 2001. Vol. 46, No. 6. p. 717-725
Publisher: Dordrecht : Kluwer Academic Publishers.
CODEN: PMBIDB; ISSN: 0167-4412
NOTE: Includes references
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

AB Plant fatty acid elongase which catalyzes very-long-chain fatty acid (VLCFA) biosynthesis is a membrane-bound multienzyme complex. It is composed of four enzymes, a 3-ketoacyl-CoA synthase (condensing enzyme), a 3-ketoacyl-CoA reductase, a 3-hydroxyacyl-CoA dehydrase, and an enoyl-CoA reductase required for completion of each step of 2-carbon elongation of fatty acids. To improve our understanding of the overall regulation of the fatty acid elongase, we investigated the spatial and temporal expression of its key component, the FAE1-condensing enzyme, and examined the activity of the promoter of the FAE1 gene in **Arabidopsis.** In situ hybridization results revealed that FAE1 transcripts were found exclusively in the embryo. RNA blot analysis and histochemical analysis of GUS activity in pFAE1::GUS transgenic **Arabidopsis** lines demonstrated that the FAE1 gene was already transcribed in the early torpedo stage embryos 4-5 days after flowering, with transcription reaching its peak 9-11 days after flowering. VLCFA deposition closely paralleled FAE1 transcript accumulation. FAE1 promoter was highly active and embryo-specific. Because its timing coincides with the period of major storage lipid accumulation, and because its in vivo activity in **Arabidopsis** is superior to the napin promoter, FAE1 promoter may be ideal for genetic engineering of seed oil composition.

L13 ANSWER 11 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2000:814628 CAPLUS
DOCUMENT NUMBER: 133:359818
TITLE: Arabidopsis KNAT411 gene **promoter** and its use for **seed-specific** gene expression in **transgenic plants**
INVENTOR(S): Terry, L. Thomas; Hsieh, Tzung-fu
PATENT ASSIGNEE(S): Rhobio, Fr.
SOURCE: PCT Int. Appl., 71 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000068388	A1	20001116	WO 2000-EP4879	20000505
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6342657	B1	20020129	US 1999-306060	19990506
CA 2370027	AA	20001116	CA 2000-2370027	20000505
EP 1177300	A1	20020206	EP 2000-931269	20000505
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.: US 1999-306060 A 19990506
WO 2000-EP4879 W 20000505

AB The present invention is directed to isolated **promoter** sequences from **seed-specific** genes, such as KNAT411 . When operably linked to either the coding sequence of a heterologous gene or a sequence complementary to a native plant gene, the subject promoters direct expression of the coding sequence or complementary sequence in a plant seed, including the early embryo. The promoter sequences are useful in expression cassettes and expression vectors for the **transformation** of **plants.** Also provided are methods of directing seed-specific expression of a gene or sequence complementary to a native plant gene by introducing into a plant cell an isolated nucleic acid comprising a subject promoter operably linked to said gene or complementary sequence. Methods for activating a site-specific recombination system in the early embryo of a seed by **transforming** a **plant** with an expression cassette comprising a subject promoter operably linked to a recombinase gene are also provided. Thus, the **A. thaliana** KNAT411 gene promoter was cloned and sequenced. This gene was found to be active very early in embryogenesis, much earlier than other known **seed-specific promoters.** Southern anal. indicated that there was only one KNAT411 gene, but there were several KNAT411-like sequences in the **A. thaliana** genome. The KNAT411 gene was determined to have five exons separated by four introns. The observed position of the third intron (inside the ELK domain) and of the fourth intron (interrupting the homeodomain) is characteristic of knotted genes.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:421296 CAPLUS
DOCUMENT NUMBER: 133:70692
TITLE: Fatty acyl-CoA:fatty alcohol acyltransferases from jojoba and Arabidopsis
INVENTOR(S): Lardizabal, Kathryn Dennis; Metz, James George; Lassner, Michael W.
PATENT ASSIGNEE(S): Calgene Llc, USA
SOURCE: PCT Int. Appl., 102 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 12
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000036095	A2	20000622	WO 1999-US28678	19991203
WO 2000036095	A3	20000803		
W: CA, CN, JP, KR, MX				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6492509	B1	20021210	US 1998-205815	19981204
CA 2352473	AA	20000622	CA 1999-2352473	19991203
EP 1135474	A2	20010926	EP 1999-967187	19991203
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2002532089	T2	20021002	JP 2000-588344	19991203

PRIORITY APPLN. INFO.:

US 1998-205815	A	19981204
US 1994-265047	A1	19940623
US 1997-48651P	P	19970605
US 1998-92562	A2	19980605
WO 1998-US11590	A2	19980605
WO 1999-US28678	W	19991203

AB By this invention, nucleic acid sequences encoding for fatty acyl-CoA:fatty alc. acyltransferase (wax synthase, EC 2.3.1.75) are provided from jojoba (Simmondsia chinensis) and Arabidopsis thaliana, wherein said wax synthase is active in the formation of a wax ester from fatty alc. and fatty acyl-CoA substrates. Of special interest are nucleic acid sequences obtainable from a jojoba embryo wax synthase having an apparent mol. mass of .apprx.33 kDa. Also provided are 7 repeats of an **A. thaliana** genomic sequence with similarity to jojoba wax synthase. Also considered are amino acid and nucleic acid sequences obtainable from wax synthase proteins and the use of such sequences to provide transgenic host cells capable of producing wax esters. Methods of producing wax esters in a plant cell by expressing a heterologous cDNA sequence encoding fatty acyl acyltransferase are described. The invention also provides plant cells containing wax ester, and novel oil compns. and was compns. comprising 40:2 wax ester as a predominant component.

L13 ANSWER 13 OF 24 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
ACCESSION NUMBER: 2001:198654 BIOSIS
DOCUMENT NUMBER: PREV200100198654
TITLE: Inhibition of polyunsaturated fatty acid accumulation in plants expressing a fatty acid epoxygenase.
AUTHOR(S): Singh, S. [Reprint author]; Thomaeus, S.; Lee, M.; Green, A.; Stymne, S.
CORPORATE SOURCE: CSIRO Plant Industry, Canberra, ACT, Australia surinder.singh@pi.csiro.au
SOURCE: Biochemical Society Transactions, (December, 2000) Vol. 28, No. 6, pp. 940-942. print.
CODEN: BCSTB5. ISSN: 0300-5127.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 25 Apr 2001
Last Updated on STN: 18 Feb 2002

AB Earlier, we described the isolation of a Crepis palaestina cDNA (Cpal2) which encoded a DELTA12-epoxygenase that could catalyse the synthesis of

12,13-epoxy-cis-9-octadecenoic acid (18:1E) from linoleic acid (18:2). When the Cpal2 gene was expressed under the control of a **seed** -specific **promoter** in **Arabidopsis**, plants were able to accumulate small amounts 18:1E and 12,13-epoxy-cis-9,15-octadec-2-enoic acid in their seed lipids. In this report we give results obtained from a detailed analysis of **transgenic Arabidopsis** **plants** containing the Cpal2 gene. The seeds from these plants accumulate varying levels of 18:1E, but show a marked increase in 18:1 and equivalent decrease in 18:2 and 18:3. We further observed that the co-expression of a C. palaestina DELTA12-desaturase in **Arabidopsis** appears to return the relative proportions of the C18 seed fatty acids to normal levels and results in a 2-fold increase in total epoxy fatty acids.

L13 ANSWER 14 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN

ACCESSION NUMBER: 1998:75735 AGRICOLA
DOCUMENT NUMBER: IND21641427
TITLE: Evaluation of genes to reduce seed size in **Arabidopsis** and tobacco and their application to Citrus. [Erratum: 1998, v. 4 (6), p. 559.]
AUTHOR(S): Koltunow, A.M.; Brennan, P.; Bond, J.E.; Barker, S.J.
CORPORATE SOURCE: CSIRO Plant Industry, Glen Osmond, South Australia.
AVAILABILITY: DNAL (QK981.4.M63)
SOURCE: Molecular breeding : new strategies in plant improvement, 1998. Vol. 4, No. 3. p. 235-251
Publisher: Dordrecht ; Boston : Kluwer Academic Publishers, c1995-
CODEN: MOBRFL; ISSN: 1380-3743
NOTE: Includes references
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

AB Seedlessness is a highly desirable characteristic in fresh fruit. Marketability of a fruit as seedless does not require complete absence of seeds as long as the seed structures are imperceptible during consumption. Chimaeric genes comprised of soybean beta-conglycinin **seed** storage protein gene **promoters** linked to the bacterial RNase gene, Barnase, were tested for their efficacy to cause seed death and decrease seed size in tobacco and **Arabidopsis.** These species were used because they undergo two distinct seed developmental pathways and produce albuminous and exalbuminous seeds, respectively. In both species, the death of embryo and endosperm tissues occurred, resulting in a dominant seed lethal phenotype with segregation distortion. Reduction in seed size was only observed in **Arabidopsis** seeds and the phenotype resembled that of stenospermocarpic seeds in grape. Some transformants of both species were male-sterile and this correlated with the expression of the gene in anthers indicating that expression of the gene is not strictly **seed**-specific. The **promoters** also direct expression of a linked GUS gene to Citrus embryos of various developmental stages, and Citrus forms exalbuminous seeds, therefore, the Barnase constructions may be useful in eliciting a reduction in seed size of around 75% of the seeds found in the fruit. This may be sufficient to warrant marketing as 'less seedy' if trials in the cultivar of interest indicate that the smaller seeds are less detectable to the consumer.

L13 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:628343 CAPLUS

DOCUMENT NUMBER: 129:340310
TITLE: Comparison of sense and antisense methodologies for modifying the fatty acid composition of Arabidopsis thaliana oilseed
AUTHOR(S): Cartea, M. E.; Migdal, M.; Galle, A. M.; Pelletier, G.; Guerche, P.
CORPORATE SOURCE: Station de Genetique et d'Amelioration des plantes INRA, Versailles, F-78026, Fr.
SOURCE: Plant Science (Shannon, Ireland) (1998), 136(2), 181-194
CODEN: PLSCE4; ISSN: 0168-9452
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The industrial usefulness and nutritional value of vegetable oils can be improved by modifying the levels of certain polyunsatd. fatty acids. In the developing embryo of oilseed plants, the degree of saturation of C18 fatty acids is mainly controlled by the activity of the microsomal Δ12 and Δ15 desaturases. We have constructed chimeric genes using a **seed-specific promoter** (AT2S2) and the coding sequences from Arabidopsis Δ12 or rapeseed Δ15 desaturases in two orientations in order to define the most efficient way to specifically modify the fatty acid composition of transgenic Arabidopsis thaliana seeds. Homozygous lines derived from > 100 independent **transgenic** Arabidopsis **plants** were selected for the four constructs. Oil from their seeds shows significant modifications of oleic, linoleic and α-linolenic acid content when compared with oil from the control plants. The sense strategy led mainly to an overexpression of the desaturase activity and in some cases to its inhibition, presumably by co-suppression or sense-suppression of the endogenous genes, while the antisense strategy gave a graded range of activity. These results highlight the advantages and limits of both strategies and complement results from work in soybean and rapeseed plants. Fatty acid synthesis during **A. thaliana** seed formation is a potentially useful model for production of other oils through modified desatn. patterns, including industrial oils with hydroxy, epoxy or elongated fatty acids.

REFERENCE COUNT: 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 16 OF 24 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
ACCESSION NUMBER: 1998:46243 BIOSIS
DOCUMENT NUMBER: PREV199800046243
TITLE: **Arabidopsis** thaliana class IV chitinase is early induced during the interaction with Xanthomonas campestris.
AUTHOR(S): Gerhardt, Liliane B. De A.; Sachetto-Martins, Gilberto; Contarini, Maria G.; Sandroni, Mariana; Ferreira, Rodrigo De P.; Lima, Viviane M. De; Cordeiro, Maria C.; Oliveira, Dulce E. De; Margis-Pinheiro, Marcia [Reprint author]
CORPORATE SOURCE: Lab. Genet. Mol. Veg., Dep. Genet., Univ. Fed. Rio de Janeiro, CP 6811, CEP 21941-970 Rio de Janeiro, RJ, Brazil
SOURCE: FEBS Letters, (Dec. 8, 1997) Vol. 419, No. 1, pp. 69-75. print.
CODEN: FEBLAL. ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
OTHER SOURCE: Genbank-AC002333; Genbank-AC002335; Genbank-M38240
ENTRY DATE: Entered STN: 27 Jan 1998
Last Updated on STN: 27 Jan 1998

AB Endochitinases are widely distributed among higher plants, including a

number of important crop species. They are generally considered to be involved in plant defence against potential pathogens. We have cloned a class IV chitinase gene (AtchitIV) from **Arabidopsis** thaliana. Southern blot analysis allowed the detection of two cross-hybridizing genes in the **A. thaliana** genome. AtchitIV transcripts are detected in seedpods, but not in roots, inflorescence stems, leaves and flowers of healthy plants. The transcripts accumulated very rapidly in leaves after inoculation with Xanthomonas campestris. Maximum mRNA accumulation was reached one hour after infection and decreased to very low levels 72 hours after induction. This result suggests an involvement of AtchitIV in the initial events of the hypersensitive reaction. Nevertheless, **A. thaliana plants transformed** with the gus gene under the control of a class IV chitinase bean **promoter**, showed GUS activity in **seed** embryos. These data, together with the constitutive expression of the endogenous gene in the seedpods, points to additional physiological roles for this protein.

L13 ANSWER 17 OF 24 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 2

ACCESSION NUMBER: 1996:268108 BIOSIS
DOCUMENT NUMBER: PREV199698824237
TITLE: **DNA** sequences that activate isocitrate lyase gene expression during late embryogenesis and during postgerminative growth.
AUTHOR(S): Zhang, James Z.; Santes, Cristina M.; Engel, Michele L.; Gasser, Charles S.; Harada, John J. [Reprint author]
CORPORATE SOURCE: Sections Plant Biol., Div. Biol. Sci., Univ. California, Davis, CA 95616, USA
SOURCE: Plant Physiology (Rockville), (1996) Vol. 110, No. 4, pp. 1069-1079.
CODEN: PLPHAY. ISSN: 0032-0889.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 10 Jun 1996
Last Updated on STN: 10 Jun 1996

AB We analyzed **DNA** sequences that regulate the expression of an isocitrate lyase gene from Brassica napus L. during late embryogenesis and during postgerminative growth to determine whether glyoxysomal function is induced by a common mechanism at different developmental stages. beta-Glucuronidase constructs were used both in transient expression assays in B. napus and in transgenic **Arabidopsis** thaliana to identify the segments of the isocitrate lyase 5' flanking region that influence promoter activity. **DNA** sequences that play the principal role in activating the promoter during postgerminative growth are located more than 1200 hp upstream of the gene. Distinct **DNA** sequences that were sufficient for high-level expression during late embryogenesis but only low-level expression during postgerminative growth were also identified. Other parts of the 5' flanking region increased **promoter** activity both in developing **seed** and in seedlings. We conclude that a combination of elements is involved in regulating the isocitrate lyase gene and that distinct **DNA** sequences play primary roles in activating the gene in embryos and in seedlings. These findings suggest that different signals contribute to the induction of glyoxysomal function during these two developmental stages. We also showed that some of the constructs were expressed differently in transient expression assays and in **transgenic plants.**

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STN DUPLICATE 3
ACCESSION NUMBER: 1995:172278 BIOSIS
DOCUMENT NUMBER: PREV199598186578
TITLE: Identification of domains in an **Arabidopsis** acyl carrier protein gene promoter required for maximal organ-specific expression.
AUTHOR(S): Baerson, Scott R.; Vander Heiden, Matthew G.; Lamppa, Gayle K. [Reprint author]
CORPORATE SOURCE: Dep. Mol. Genetics Cell Biol., Univ. Chicago, 920 E. 58th St., Chicago, IL 60637, USA
SOURCE: Plant Molecular Biology, (1994) Vol. 26, No. 6, pp. 1947-1959.
CODEN: PMBIDB. ISSN: 0167-4412.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Apr 1995
Last Updated on STN: 26 Apr 1995

AB Deletions were made in the promoter of the acyl carrier protein (ACP) Acl1.2 gene from **Arabidopsis** to investigate the nature of the cis-acting elements that direct its expression. These constructs, which included the untranslated leader region, were fused to a reporter gene coding for beta-glucuronidase (GUS) and transformed into tobacco. Quantitative fluorometric analysis of GUS activity in **transgenic plants** showed that expression in young leaves drops to a basal level when a 85 hp domain, from -320 to -236 relative to transcription initiation, is deleted. Maximum promoter activity in roots also depends on this domain, but two other regions are also important. In total, deletion of the sequences from -466 to -55 caused an ca. 80-fold reduction in Acl1.2 promoter activity in roots. The -320 to -236 domain forms a complex with a protein factor found in leaves and roots, which was not detectable in seeds. The formation of this protein-**DNA** complex was abolished by mutation of a bZIP core motif, ACGT, found within the context AAGACGTAG, which is dissimilar to the other bZIP-binding sites thus far characterized in plants. Previously we showed that Acl1.2 **promoter** activity is highest in **seeds** (2). Here we find, in contrast to leaves and roots, that deletion to position -236 has no effect on GUS levels in seeds. However, nearly a 100-fold drop was observed when the -235 to -55 region was removed. Hence, this 180 hp domain contains all the cis-acting information necessary for Acl1.2 **promoter** activity in **seeds.** The same region is necessary for Acl1.2 activity in the receptacle, stigma, tapetum and pollen of the flower, as demonstrated by histochemical staining.

L13 ANSWER 19 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
ACCESSION NUMBER: 94:59106 AGRICOLA
DOCUMENT NUMBER: IND20409898
TITLE: Regulation of the rab17 gene promoter in transgenic **Arabidopsis** wild-type, ABA-deficient and ABA-insensitive mutants.
AUTHOR(S): Vilardell, J.; Martinez-Zapater, J.M.; Goday, A.; Pages, M.
AVAILABILITY: DNAL (QK710.P62)
SOURCE: Plant molecular biology, Feb 1994. Vol. 24, No. 4. p. 561-569
Publisher: Dordrecht : Kluwer Academic Publishers.
CODEN: PMBIDB; ISSN: 0167-4412
NOTE: Includes references

PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

AB The abscisic acid-responsive gene rab17 is induced during maize embryo maturation and in vegetative tissues under water stress conditions. To investigate how ABA is involved in the induction of the rab17 gene, we present here a genetic approach to analyse the transcriptional regulation of the 1.3 kb rab17 promoter fragment in transgenic wild-type **Arabidopsis** and mutants which are deficient (aba) and insensitive (abi1, abi2 and abi3) to ABA. During **seed** development the rab17 **promoter** fragment confers similar temporal and spatial regulation on the reporter gene GUS, both in transgenic wild-type and ABA-deficient and ABA-insensitive mutants. The rab17 promoter was only active in embryo and endosperm during late seed development, although the ABA-deficient embryo mutant showed a reduction in the level of GUS activity. During germination rab17 promoter activity decreases, and GUS activity is not enhanced by water stress in **transgenic** wild-type and mutant **plants.** In contrast, transcription of the **Arabidopsis** endogenous rab gene is stimulated by water stress, both in wild-type and ABA-insensitive mutants. Our data suggest that different molecular mechanisms mediate seed-specific expression and ABA water stress induction of the rab17 gene and indicate strong conservation of the seed-specific regulatory mechanism for rab genes in monocot and dicot plants.

L13 ANSWER 20 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN

ACCESSION NUMBER: 94:74687 AGRICOLA
DOCUMENT NUMBER: IND20422622
TITLE: Regulation of an **Arabidopsis** oleosin gene promoter in transgenic Brassica napus.
AUTHOR(S): Plant, A.L.; Van Rooijen, G.J.H.; Anderson, C.P.; Moloney, M.M.
AVAILABILITY: DNAL (QK710.P62)
SOURCE: Plant molecular biology, May 1994. Vol. 25, No. 2. p. 193-205
Publisher: Dordrecht : Kluwer Academic Publishers.
CODEN: PMBIDB; ISSN: 0167-4412
NOTE: Includes references
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English

AB Progressive deletions of the 5'-flanking sequences of an **Arabidopsis** oleosin gene were fused to beta-glucuronidase (GUS) and introduced into Brassica napus **plants** using Agrobacterium-mediated **transformation.** The effect of these deletions on the quantitative level of gene expression, organ specificity and developmental regulation was assessed. In addition, the influence of abscisic acid (ABA), jasmonic acid (JA), sorbitol and a combined ABA/sorbitol treatment on gene expression was investigated. Sequences that positively regulate quantitative levels of gene expression are present between - 1100 to -600 and -400 to -200 of the promoter. In addition, sequences present between -600 and -400 down-regulate quantitative levels of expression. In **transgenic** B. napus **plants**, the oleosin **promoter** directs **seed** -specific expression of GUS which is present at early stages of seed development and increases throughout seed maturation. Sequences present

between -2500 and -1100 of the promoter are involved in modulating the levels of expression at early stages of embryo development. Histochemical staining of embryos demonstrated that expression is uniform throughout the tissues of the embryo. Sequences involved in the response to ABA and sorbitol are present between -400 and -200. The induction of GUS activity by a combined ABA/sorbitol treatment is additive suggesting that ABA is not the sole mediator of osmotically induced oleosin gene expression. A response to JA was only observed when the oleosin promoter was truncated to -600 suggesting that the reported effect of JA on oleosin gene expression may be at a post-transcriptional level.

L13 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1992:1651 CAPLUS
DOCUMENT NUMBER: 116:1651
TITLE: A novel seed protein gene from Vicia faba is developmentally regulated in **transgenic** tobacco and Arabidopsis **plants**
AUTHOR(S): Baeumlein, Helmut; Boerjan, Wout; Nagy, Istvan; Bassuener, Ronald; Van Montagu, Marc; Inze, Dirk; Wobus, Ulrich
CORPORATE SOURCE: Zentralinst. Genet. Kulturpflanzenforsch., Akad. Wiss. DDR, Gatersleben, O-4325, Germany
SOURCE: Molecular and General Genetics (1991), 225(3), 459-67
CODEN: MGGEAE; ISSN: 0026-8925
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A novel gene, denoted USP, was isolated from V. faba var. minor, which corresponds to the most abundant mRNA present in cotyledons during early seed development; however, the corresponding protein does not accumulate in cotyledons. The characterized USP gene with its 2 introns is 1 of about 15 members of a gene family. A fragment comprising 637 bp of 5' flanking sequence and the total 5' untranslated region was shown to be sufficient to drive the mainly seed-specific expression of 2 reporter genes, coding for neomycin phosphotransferase II and β-glucuronidase, in transgenic **A. thaliana** and Nicotiana tabacum plants. The USP promoter was active in transgenic tobacco seeds in both the embryo and the endosperm, whereas its activity in Arabidopsis was detectable only in the embryo. Moreover, a transient activity pattern of the USP promoter was demonstrated in root tips of both transgenic host species.

L13 ANSWER 22 OF 24 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
ACCESSION NUMBER: 2004:7979 AGRICOLA
DOCUMENT NUMBER: IND43615141
TITLE: Synthesis of ketocarotenoids in the seed of **Arabidopsis** thaliana.
AUTHOR(S): Stalberg, K.; Lindgren, O.; Ek, B.; Hoglund, A.S.
AVAILABILITY: DNAL (QK710.P68)
SOURCE: Plant journal, p. 771-779
ISSN: 0960-7412
NOTE: Includes references
DOCUMENT TYPE: Article
FILE SEGMENT: Non US
LANGUAGE: English
AB A cDNA coding for a gene necessary for synthesis of ketocarotenoids was cloned from the alga Haematococcus pluvialis and expressed in the seed of **Arabidopsis** thaliana. The expression of the algal

(beta)-carotene-oxygenase gene was directed to the seed by use of the 2S, **seed** storage protein **promoter** napA. Extracts from **seeds** of the **transgenic plants** were clearly red because of accumulation of ketocarotenoids, and free and esterified forms of ketocarotenoids were found in addition to the normal carotenoid composition in the seed. The major ketocarotenoids in the **transgenic plants** were: 4-keto-lutein (3,3'-dihydroxy-(beta)-,epsilon-carotene-4-one), adonirubin (3-hydroxy-(beta)-,(beta)-carotene-4,4'-dione) and canthaxanthin ((beta)-(beta),'-carotene-4,4'-dione). 4-Keto-lutein differs from the more common adonixanthin only in the position of one double bond. To increase the substrate availability for the (beta)-carotene-oxygenase, these **transformants** were crossed with **transgenic plants** overexpressing a construct of an endogenous phytoene synthase gene, also under the control of the napA promoter. The resulting crossings gave rise to seeds with a 4.6-fold relative increase of the total pigment, and the three major ketocarotenoids were increased 13-fold compared to seeds of **transgenic plants** carrying only the (beta)-carotene-oxygenase construct.

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ACCESSION NUMBER: 2004:10160 AGRICOLA
DOCUMENT NUMBER: IND43617544
TITLE: Repression of gene expression by **Arabidopsis** HD2 histone deacetylases.
AUTHOR(S): Wu, K.; Tian, L.; Zhou, C.; Brown, D.; Miki, B.
AVAILABILITY: DNAL (QK710.P68)
SOURCE: Plant journal, p. 241-247
ISSN: 0960-7412
NOTE: Includes references
DOCUMENT TYPE: Article
FILE SEGMENT: Non US
LANGUAGE: English

AB The four HD2 proteins of **Arabidopsis** thaliana (AtHD2A-D) belong to a unique class of histone deacetylases that is plant specific. Previously, we have demonstrated that one of the members, AtHD2A, can mediate transcriptional repression when targeted to the promoter of a reporter gene. Here, we report that AtHD2B and AtHD2C can also repress gene expression. AtHD2A and AtHD2C differ from AtHD2B and AtHD2D in the composition of their structural domains. Our data show that both structural types play a role in the repression of gene transcription. We demonstrate that AtHD2A can mediate gene repression through interactions with transcription factors in plants. By fusing AtHD2A with the **DNA**-binding domain of the plant transcriptional factor Pti4, the expression of a GCC box containing reporter gene was repressed. We also demonstrated repression of a GUS gene with GAL4 enhancers using **transgenic plants** that expressed a GAL4/AtHD2A fusion gene. Furthermore, the expression of the GAL4/AtHD2A protein using the **seed**-specific napin **promoter** (NAP2) and the constitutive tCUP promoter demonstrated that repression of transgenes could be achieved in a tissue-specific or unrestricted manner. Targeting of HD2 proteins to specific promoters using transcription factor **DNA**-binding domains may therefore provide a new technology for silencing target genes and pathways in plants as well as for assessing the function of unknown transcription factors.

L13 ANSWER 24 OF 24 AGRICOLA Compiled and distributed by the National

ACCESSION NUMBER: 2004:33031 AGRICOLA
DOCUMENT NUMBER: IND43634008
TITLE: The 5' UTR negatively regulates quantitative and spatial expression from the ABI3 promoter.
AUTHOR(S): Ng, D.W.K.; Chandrasekharan, M.B.; Hall, T.C.
AVAILABILITY: DNAL (QK710.P62)
SOURCE: Plant molecular biology, p. 25-38
ISSN: 0167-4412
NOTE: Includes references
DOCUMENT TYPE: Article
FILE SEGMENT: Non-US
LANGUAGE: English

AB The involvement of transcription factors **Arabidopsis** abscisic acid-insensitive3 (ABI3), maize viviparous1 (VP1) and Phaseolus vulgaris ABI3-like factor (PvALF) in the spatial control of storage protein gene expression is well established. However, little insight exists as to how they are themselves regulated. To address this, a 5.15 kb ABI3 upstream sequence including a 4.6 kb full-length promoter and 519 bp of 5'-untranslated region (UTR) was used to drive either beta-glucuronidase (GUS) or green fluorescent protein (GFP) expression in **Arabidopsis** . Expression from the full-length (-4630/+519ABI3) and various 5'-truncated promoters was detected during embryogenesis in all lines, except those transgenic for promoter elements shorter than 364 bp. Two upstream activating regions, -3600 to -2033 and -2033 to -882, enhanced GUS expression in seeds. The -882 to -364 region was sufficient to confer seed-specific expression of GUS when fused to a -64/+6CaMV 35S minimal promoter. Expression from the ABI3 **promoter** constructs was **seed**-specific, except in the presence of exogenous abscisic acid (ABA) (>0.3 micromolar), when GUS expression was detected in seedling roots. Excision of a 405 bp region containing three upstream open reading frames (uORFs) from the 5'-UTR dramatically increased GUS expression and debilitated constraint of reporter expression in roots. Negative regulation of ABI3 expression by the 5'-UTR may involve a post-transcriptional mechanism analogous to that of tumor suppressor genes which also bear long, uORF-containing, 5'-UTRs, or through interactions with RNA-binding proteins.

=>

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L5	96	seed adj3 promoter adj3 sequence	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/12/07 16:05
L6	51	l5 and arabidopsis adj thaliana	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/12/07 16:06
L7	27	l6 and GUS	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/12/07 16:07
L8	24	L7 and seed adj2 specific	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/12/07 16:07
L9	24	l8 and (DNA or nucleotide sequence)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2004/12/07 16:08